

ZYU.0603.ST25.txt  
SEQUENCE LISTING

<110> Yu, Zailin

Fu, Yan

<120> RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLOGICAL EFFECTS

<130> ZYU-0603

<150> US 06/392,948

<151> 2002-07-01

<160> 40

<170> PatentIn version 3.1

<210> 1

<211> 2229

<212> DNA

<213> Artificial Sequence

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<223> DNA of HSA-hIL-11

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## ZYU.0603.ST25.txt

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| tgctgtttgc caaagctcga tgaacttcgg gatgaaggga aggcttcgtc tgccaaacag  | 660  |
| agactcaagt gtgccagtct ccaaaaatth ggagaaagag ctttcaaagc atgggcagta  | 720  |
| gctcgcctga gccagagatt tcccaaagct gagtttgag aagtttccaa gttagtga     | 780  |
| gatcttacca aagtccacac ggaatgctgc catggagatc tgcttgaatg tgctgatgac  | 840  |
| agggcggacc ttgccaagta tatctgtgaa aatcaagatt cgatctccag taaactgaag  | 900  |
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| gagatgcctg ctgacttgcc ttcattagct gctgattttg ttgaaagtaa ggatgtttgc  | 1020 |
| aaaaactatg ctgaggcaaa ggatgtcttc ctgggcatgt ttttgatga atatgcaaga   | 1080 |
| aggcatcctg attactctgt cgtgctgctg ctgagacttg ccaagacata tgaaaccact  | 1140 |
| ctagagaagt gctgtgccgc tgcagatcct catgaatgct atgccaaagt gttcgatgaa  | 1200 |
| tttaaaccctc ttgtggaaga gcctcagaat ttaatcaaac aaaattgtga gctttttgag | 1260 |
| cagcttgag agtacaaatt ccagaatgcg ctattagttc gttacaccaa gaaagtacc    | 1320 |
| caagtgtcaa ctccaactct tgtagaggct tcaagaaacc taggaaaagt gggcagcaaa  | 1380 |
| tggtgtaaac atcctgaagc aaaaagaatg ccctgtgcag aagactatct atccgtggc   | 1440 |
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| tgacagaaat ccttggtgaa caggcgacca tgcttttcag ctctggaagt cgatgaaaca  | 1560 |
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| cccaaggcaa caaaagagca actgaaagct gttatggatg atttcgcagc ttttgtagag  | 1740 |
| aagtgtgca aggtgacga taaggagacc tgctttgccg aggagggtaa aaaacttgtt    | 1800 |
| gctgcaagtc aagctgcctt aggcttagct cccatgacct agacaacgtc cttgaagaca  | 1860 |
| agctgggtta actgctctaa catgatcgat gaaattataa cactttaaa gcagccacct   | 1920 |
| ttgcctttgc tggacttcaa caacctcaat ggggaagacc aagacattct gatggaaaat  | 1980 |
| aaccttcgaa ggccaaacct ggaggcattc aacagggtcg tcaagagttt acagaacgca  | 2040 |
| tcagcaattg agagcattct taaaaatctc ctgccatgtc tgcccctggc cacggccgca  | 2100 |
| cccacgcgac atccaatcca tatcaaggac ggtgactgga atgaattccg gaggaaactg  | 2160 |
| acgttctatc tgaaaaccct tgagaatgcg caggctcaac agacgacttt ggcctcgcg   | 2220 |
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<223> HSA-hIL-11

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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
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Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
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Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
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Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
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Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
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Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
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Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
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 210 215 220  
 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys  
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 260 265 270  
 Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His  
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 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser  
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 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg  
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Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala-Asp  
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Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala  
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Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val  
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Leu Thr Arg Ser Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu  
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Arg Asp Lys Phe Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro  
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Thr Leu Ala Met Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly  
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Val Leu Thr Arg Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val  
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Gln Trp Leu Arg Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro  
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Glu Leu Gly Thr Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu  
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Gln Leu Leu Met Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro  
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Pro Ala Pro Pro Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg  
 725 730 735

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<212> DNA

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| gaaaatttca aagccttggt gttgattgcc tttgctcagt atcttcagca gtgtccattt  | 180 |
| gaagatcatg taaaattagt gaatgaagta actgaatttg caaaaacatg tgttgctgat  | 240 |
| gagtcagctg aaaattgtga caaatcactt catacccttt ttggagacaa attatgcaca  | 300 |
| gttgcaactc ttcgtgaaac ctatggtgaa atggctgact gctgtgcaaa acaagaacct  | 360 |
| gagagaaatg aatgcttctt gcaacacaaa gatgacaacc caaacctccc ccgattgggtg | 420 |
| agaccagagg ttgatgtgat gtgcactgct tttcatgaca atgaagagac atttttgaaa  | 480 |
| aaatacttat atgaaattgc cagaagacat ccttactttt atgccccgga actccttttc  | 540 |
| tttgctaaaa ggtataaagc tgctttttaca gaatgttgcc aagctgctga taaagctgcc | 600 |
| tgctgtttgc caaagctcga tgaacttcgg gatgaaggga aggcttcgtc tgccaaacag  | 660 |
| agactcaagt gtgccagtct ccaaaaattt ggagaaagag ctttcaaagc atgggcagta  | 720 |
| gctcgcctga gccagagatt tcccaaagct gagtttgagc aagtttccaa gttagtgcac  | 780 |
| gatcttacca aagtccacac ggaatgctgc catggagatc tgcttgaatg tgctgatgac  | 840 |
| agggcggacc ttgccaagta tatctgtgaa aatcaagatt cgatctccag taaactgaag  | 900 |

## ZYU.0603.ST25.txt

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&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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&lt;223&gt; HSA-hIL-3

&lt;400&gt; 4

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 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
 35 40 45  
 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
 50 55 60  
 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
 65 70 75 80  
 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
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 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
 100 105 110  
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 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
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 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
 165 170 175  
 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
 180 185 190  
 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
 195 200 205  
 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
 210 215 220  
 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys  
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 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp  
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Cys Ile Ala Glu Val Glu Asn<sub>295</sub> Asp Glu Met Pro Ala<sub>300</sub> Asp Leu Pro Ser

Leu<sub>305</sub> Ala Ala Asp Phe Val<sub>310</sub> Glu Ser Lys Asp Val<sub>315</sub> Cys Lys Asn Tyr Ala<sub>320</sub>

Glu Ala Lys Asp Val<sub>325</sub> Phe Leu Gly Met Phe<sub>330</sub> Leu Tyr Glu Tyr Ala<sub>335</sub> Arg

Arg His Pro Asp<sub>340</sub> Tyr Ser Val Val<sub>345</sub> Leu Leu Arg Leu Ala<sub>350</sub> Lys Thr

Tyr Glu Thr<sub>355</sub> Thr Leu Glu Lys Cys<sub>360</sub> Cys Ala Ala Ala Asp<sub>365</sub> Pro His Glu

Cys Tyr Ala Lys Val Phe Asp<sub>375</sub> Glu Phe Lys Pro Leu<sub>380</sub> Val Glu Glu Pro

Gln Asn Leu Ile Lys Gln<sub>390</sub> Asn Cys Glu Leu Phe<sub>395</sub> Glu Gln Leu Gly Glu<sub>400</sub>

Tyr Lys Phe Gln Asn<sub>405</sub> Ala Leu Leu Val Arg<sub>410</sub> Tyr Thr Lys Lys Val<sub>415</sub> Pro

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Ala Glu Asp Tyr Leu Ser Val<sub>455</sub> Val Leu Asn Gln Leu<sub>460</sub> Cys Val Leu His

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565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Pro Met Thr Gln Thr Thr  
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Ser Leu Lys Thr Ser Trp Val Asn Cys Ser Asn Met Ile Asp Glu Ile  
595 600 605

Ile Thr His Leu Lys Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn  
610 615 620

Leu Asn Gly Glu Asp Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg  
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Pro Asn Leu Glu Ala Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala  
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Ser Ala Ile Glu Ser Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu  
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Ala Thr Ala Ala Pro Thr Arg His Pro Ile His Ile Lys Asp Gly Asp  
675 680 685

Trp Asn Glu Phe Arg Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu  
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<212> DNA

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| gaaaatttca aagccttggt gttgattgcc tttgctcagt atcttcagca gtgtccattt  | 180  |
| gaagatcatg taaaattagt gaatgaagta actgaatttg caaaaacatg tgttgctgat  | 240  |
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| tttaaacctc ttgtggaaga gcctcagaat ttaatcaaac aaaattgtga gctttttgag  | 1260 |
| cagcttggag agtacaaatt ccagaatgcg ctattagttc gttacaccaa gaaagtaccc  | 1320 |
| caagtgtcaa ctccaactct tgtagaggct tcaagaaacc taggaaaagt gggcagcaaa  | 1380 |
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| ctgaaccagt tatgtgtgtt gcatgagaaa acgccagtaa gtgacagagt caccaaatgc  | 1500 |
| tgcacagaat ccttggtgaa caggcgacca tgcttttcag ctctggaagt cgatgaaaca  | 1560 |
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| tctgagaagg agagacaaat caagaaacaa actgcacttg ttgagcttgt gaaacacaag  | 1680 |
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35 40 45

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50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100

105

110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
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 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
 145 150 155 160  
 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
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 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
 180 185 190  
 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
 195 200 205  
 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
 210 215 220  
 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys  
 225 230 235 240  
 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp  
 245 250 255  
 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser  
 260 265 270  
 Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His  
 275 280 285  
 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser  
 290 295 300  
 Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala  
 305 310 315 320  
 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg  
 325 330 335  
 Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr  
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu  
 355 360 365  
 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro  
 370 375 380  
 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu  
 385 390 395 400  
 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro  
 405 410 415  
 Glu Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys  
 420 425 430  
 Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys  
 435 440 445  
 Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His  
 450 455 460  
 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser  
 465 470 475 480  
 Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr  
 485 490 495  
 Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp  
 500 505 510  
 Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala  
 515 520 525  
 Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu  
 530 535 540  
 Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys  
 545 550 555 560  
 Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val  
 565 570 575  
 Ala Ala Ser Gln Ala Ala Leu Gly Leu Ile Cys Asp Ser Arg Val Leu  
 580 585 590  
 Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly  
 595 600 605

ZYU.0603.ST25.txt

Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr  
610 615 620

Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala  
625 630 635 640

Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg  
645 650 655

Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln  
660 665 670

Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu  
675 680 685

Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala  
690 695 700

Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys  
705 710 715 720

Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr  
725 730 735

Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg  
740 745

<210> 7

<211> 2352

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA of HSA-GCSF

<400> 7

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| atgaagtggg taacctttat ttcccttctt tttctcttta gctcggctta ttccaggggt | 60  |
| gtgtttcgtc gagatgcaca caagagtgag gttgctcatc ggtttaaaga tttgggagaa | 120 |
| gaaaatttca aagccttggt gttgattgcc tttgctcagt atcttcagca gtgtccattt | 180 |
| gaagatcatg taaaattagt gaatgaagta actgaatttg caaaaacatg tgttgctgat | 240 |
| gagtcagctg aaaattgtga caaatcactt catacccttt ttggagacaa attatgcaca | 300 |
| gttgcaactc ttcgtgaaac ctatggtgaa atggctgact gctgtgcaaa acaagaacct | 360 |

## ZYU.0603.ST25.txt

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gagagaaatg aatgcttctt gcaacacaaa gatgacaacc caaacctccc ccgattggtg  | 420  |
| agaccagagg ttgatgtgat gtgactgct tttcatgaca atgaagagac atttttgaaa   | 480  |
| aaatacttat atgaaattgc cagaagacat ccttactttt atgccccgga actccttttc  | 540  |
| tttgctaaaa ggtataaagc tgctttttaca gaatgttgcc aagctgctga taaagctgcc | 600  |
| tgctgtttgc caaagctcga tgaacttcgg gatgaaggga aggcttcgtc tgccaaacag  | 660  |
| agactcaagt gtgccagtct ccaaaaattt ggagaaagag ctttcaaagc atgggcagta  | 720  |
| gctcgctga gccagagatt tcccaaagct gagtttgag aagtttccaa gttagtga      | 780  |
| gatcttacca aagtccacac ggaatgctgc catggagatc tgcttgaatg tgctgatgac  | 840  |
| agggcggacc ttgccaagta tatctgtgaa aatcaagatt cgatctccag taaactgaag  | 900  |
| gaatgctgtg aaaaacctct gttggaaaaa tcccactgca ttgccgaagt ggaaaatgat  | 960  |
| gagatgcctg ctgacttgcc ttcatagct gctgattttg ttgaaagtaa ggatgtttgc   | 1020 |
| aaaaactatg ctgaggcaaa ggatgtcttc ctgggcatgt ttttgatga atatgcaaga   | 1080 |
| aggcatcctg attactctgt cgtgctgctg ctgagacttg ccaagacata tgaaaccact  | 1140 |
| ctagagaagt gctgtgccgc tgcagatcct catgaatgct atgccaaagt gttcgatgaa  | 1200 |
| tttaaacctc ttgtggaaga gcctcagaat ttaatcaaac aaaattgtga gctttttgag  | 1260 |
| cagcttgag agtacaaatt ccagaatgcg ctattagttc gttacaccaa gaaagtaccc   | 1320 |
| caagtgtcaa ctccaactct tgtagaggtc tcaagaaacc taggaaaagt gggcagcaaa  | 1380 |
| tgttgtaaac atcctgaagc aaaaagaatg ccctgtgcag aagactatct atccgtggtc  | 1440 |
| ctgaaccagt tatgtgtgtt gcatgagaaa acgccagtaa gtgacagagt caccaaagtc  | 1500 |
| tgacagaaat ccttggtgaa caggcgacca tgcttttcag ctctggaagt cgatgaaaca  | 1560 |
| tacgttccca aagagtttaa tgctgaaaca ttcaccttc atgcagatat atgcacactt   | 1620 |
| tctgagaagg agagacaaat caagaaaca actgcacttg ttgagcttgt gaaacacaag   | 1680 |
| cccaaggcaa caaaagagca actgaaagct gttatggatg atttcgcagc ttttgtagag  | 1740 |
| aagtgtgca aggctgacga taaggagacc tgctttgccc aggagggtaa aaaacttggt   | 1800 |
| gctgcaagtc aagctgcctt aggcttaacc cccctgggcc ctgccagctc cctgccccag  | 1860 |
| agcttcctgc tcaagtgtt agagcaagt aggaagatcc agggcgatgg cgcagcgtc     | 1920 |
| caggagaagc tgtgtgccac ctacaagctg tgccacccc aggagctggt gctgctcgga   | 1980 |
| cactctctgg gcatccccct ggctccccct agcagctgcc ccagccaggc cctgcagctg  | 2040 |
| gcaggctgct tgagccaact ccatagcggc cttttcctct accaggggct cctgcaggcc  | 2100 |
| ctggaagggg tctccccga gttgggtccc accttgga cactgcagct ggacgtcgcc     | 2160 |
| gactttgcca ccaccatctg gcagcagatg gaagaactgg gaatggcccc tgccctgcag  | 2220 |



## ZYU.0603.ST25.txt

cccaccagg gtgcatgcc ggccttcgcc tctgctttcc agcgccgggc aggaggggtc 2280  
 ctagttgcct cccatctgca gagcttcctg gaggtgtcgt accgcgttct acgccacctt 2340  
 gccagccct ga 2352

<210> 8

<211> 759

<212> PRT

<213> Artificial Sequence

<220>

<223> HSA-GCSF

<400> 8

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu  
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Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln  
 20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys  
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp  
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser  
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His  
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser  
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala  
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg  
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr  
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu  
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro  
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu  
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro  
 405 410 415

ZYU.0603.ST25.txt

Glu Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys  
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys  
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His  
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser  
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr  
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp  
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala  
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu  
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys  
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val  
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Thr Pro Leu Gly Pro Ala Ser  
580 585 590

Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys  
595 600 605

Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr  
610 615 620

Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly  
625 630 635 640

Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu  
645 650 655

Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly  
660 665 670

ZYU.0603.ST25.txt

Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu  
675 680 685

Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln  
690 695 700

Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly  
705 710 715 720

Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val  
725 730 735

Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val  
740 745 750

Leu Arg His Leu Ala Gln Pro  
755

<210> 9

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA of HSA-GMCSF

<400> 9

|                                                                   |     |
|-------------------------------------------------------------------|-----|
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| gtgtttcgtc gagatgcaca caagagtgag gttgctcatc ggtttaaaga tttgggagaa | 120 |
| gaaaatttca aagccttggt gttgattgcc tttgctcagt atcttcagca gtgtccattt | 180 |
| gaagatcatg taaaattagt gaatgaagta actgaatttg caaaaacatg tgttgctgat | 240 |
| gagtcagctg aaaattgtga caaatcactt catacccttt ttggagacaa attatgcaca | 300 |
| gttgcaactc ttcgtgaaac ctatggtgaa atggctgact gctgtgcaaa acaagaacct | 360 |
| gagagaaatg aatgcttctt gcaacacaaa gatgacaacc caaacctccc ccgattggtg | 420 |
| agaccagagg ttgatgtgat gtgcactgct tttcatgaca atgaagagac atttttgaaa | 480 |
| aaatacttat atgaaattgc cagaagacat ccttactttt atgccccgga actccttttc | 540 |
| tttgctaaaa ggtataaagc tgcttttaca gaatgttgcc aagctgctga taaagctgcc | 600 |
| tgctgttgc caaagctcga tgaacttcgg gatgaaggga aggcttcgtc tgccaaacag  | 660 |

ZYU.0603.ST25.txt

|                                   |                                      |      |
|-----------------------------------|--------------------------------------|------|
| agactcaagt gtgccagtct ccaaaaat    | ttt ggagaaagag ctttcaaagc atgggcagta | 720  |
| gctcgcctga gccagagatt tcccaaagct  | gagtttgcag aagtttccaa gttagtga       | 780  |
| gatcttacca aagtccacac ggaatgctgc  | catggagatc tgcttgaatg tgctgatgac     | 840  |
| agggcggacc ttgccaaagta tatctgtgaa | aatcaagatt cgatctccag taaactgaag     | 900  |
| gaatgctgtg aaaaacctct gttggaaaaa  | tcccactgca ttgccgaagt ggaaaatgat     | 960  |
| gagatgcctg ctgacttgcc ttcattagct  | gctgattttg ttgaaagtaa ggatgtttgc     | 1020 |
| aaaaactatg ctgaggcaaa ggatgtcttc  | ctgggcatgt ttttgtatga atatgcaaga     | 1080 |
| aggcatcctg attactctgt cgtgctgctg  | ctgagacttg ccaagacata tgaaaccact     | 1140 |
| ctagagaagt gctgtgccgc tgcagatcct  | catgaatgct atgccaaagt gttcgatgaa     | 1200 |
| tttaaacctc ttgtggaaga gcctcagaat  | ttaatcaaac aaaattgtga gctttttgag     | 1260 |
| cagcttggag agtacaaatt ccagaatgcg  | ctattagtgc gttacaccaa gaaagtaccc     | 1320 |
| caagtgtcaa ctccaactct tgtagaggtc  | tcaagaaacc taggaaaagt gggcagcaaa     | 1380 |
| tgttgtaaac atcctgaagc aaaaagaatg  | ccctgtgcag aagactatct atccgtggtc     | 1440 |
| ctgaaccagt tatgtgtgtt gcatgagaaa  | acgccagtaa gtgacagagt caccaaatgc     | 1500 |
| tgcacagaat ccttgggtgaa caggcgacca | tgcttttcag ctctggaagt cgatgaaaca     | 1560 |
| tacgttccca aagagtttaa tgctgaaaca  | ttcaccttc atgcagatat atgcacactt      | 1620 |
| tctgagaagg agagacaaat caagaaacaa  | actgcacttg ttgagcttgt gaaacacaag     | 1680 |
| cccaaggcaa caaaagagca actgaaagct  | gttatggatg atttcgcagc ttttgtagag     | 1740 |
| aagtgtgca aggctgacga taaggagacc   | tgctttgccg aggagggtaa aaaacttggt     | 1800 |
| gctgcaagtc aagctgcctt aggcttagca  | cccgccgct cggccagccc cagcacgcag      | 1860 |
| ccctgggagc atgtgaatgc catccaggag  | gcccggcgct tcctgaacct gagtagagac     | 1920 |
| actgctgctg agatgaatga aacagtagaa  | gtcatctcag aaatgtttga cctccaggag     | 1980 |
| ccgacctgcc tacagacccg cctggagctg  | tacaagcagg gcctgcgggg cagcctcacc     | 2040 |
| aagctcaagg gccccttgac catgatggcc  | agccactaca agcagcactg ccctccaacc     | 2100 |
| ccggaaactt cctgtgcaac ccagattatc  | acctttgaaa gtttcaaaga gaacctgaag     | 2160 |
| gactttctgc ttgtcatccc ctttgactgc  | tgggagccag tccaggagtg a              | 2211 |

<210> 10

<211> 712

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; HSA-GMCSF

&lt;400&gt; 10

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu  
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln  
 20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys  
 Page 22

225 230 240  
Val His Thr Glu Cys<sub>245</sub> Cys His Gly Asp Leu<sub>250</sub> Leu Glu Cys Ala Asp<sub>255</sub> Asp  
Arg Ala Asp Leu<sub>260</sub> Ala Lys Tyr Ile Cys<sub>265</sub> Glu Asn Gln Asp Ser<sub>270</sub> Ile Ser  
Ser Lys Leu<sub>275</sub> Lys Glu Cys Cys Glu<sub>280</sub> Lys Pro Leu Leu Glu<sub>285</sub> Lys Ser His  
Cys Ile Ala Glu Val Glu Asn<sub>295</sub> Asp Glu Met Pro Ala<sub>300</sub> Asp Leu Pro Ser  
Leu<sub>305</sub> Ala Ala Asp Phe Val<sub>310</sub> Glu Ser Lys Asp Val<sub>315</sub> Cys Lys Asn Tyr Ala<sub>320</sub>  
Glu Ala Lys Asp Val<sub>325</sub> Phe Leu Gly Met Phe<sub>330</sub> Leu Tyr Glu Tyr Ala<sub>335</sub> Arg  
Arg His Pro Asp<sub>340</sub> Tyr Ser Val Val<sub>345</sub> Leu Leu Leu Arg Leu Ala<sub>350</sub> Lys Thr  
Tyr Glu Thr<sub>355</sub> Thr Leu Glu Lys Cys<sub>360</sub> Cys Ala Ala Ala Asp<sub>365</sub> Pro His Glu  
Cys Tyr Ala Lys Val Phe Asp<sub>375</sub> Glu Phe Lys Pro Leu<sub>380</sub> Val Glu Glu Pro  
Gln Asn Leu Ile Lys Gln<sub>390</sub> Asn Cys Glu Leu Phe<sub>395</sub> Glu Gln Leu Gly Glu<sub>400</sub>  
Tyr Lys Phe Gln Asn<sub>405</sub> Ala Leu Leu Val Arg<sub>410</sub> Tyr Thr Lys Lys Val<sub>415</sub> Pro  
Glu Val Ser Thr<sub>420</sub> Pro Thr Leu Val Glu<sub>425</sub> Val Ser Arg Asn Leu<sub>430</sub> Gly Lys  
Val Gly Ser<sub>435</sub> Lys Cys Cys Lys His<sub>440</sub> Pro Glu Ala Lys Arg<sub>445</sub> Met Pro Cys  
Ala Glu Asp Tyr Leu Ser Val<sub>455</sub> Val Leu Asn Gln Leu<sub>460</sub> Cys Val Leu His  
Glu Lys Thr Pro Val Ser<sub>470</sub> Asp Arg Val Thr Lys<sub>475</sub> Cys Cys Thr Glu Ser<sub>480</sub>

ZYU.0603.ST25.txt

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr  
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp  
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala  
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu  
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys  
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val  
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Pro Ala Arg Ser Pro Ser  
580 585 590

Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu Ala Arg  
595 600 605

Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr  
610 615 620

Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu  
625 630 635 640

Gln Thr Arg Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr  
645 650 655

Lys Leu Lys Gly Pro Leu Thr Met Met Ala Ser His Tyr Lys Gln His  
660 665 670

Cys Pro Pro Thr Pro Glu Thr Ser Cys Ala Thr Gln Ile Ile Thr Phe  
675 680 685

Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu Leu Val Ile Pro Phe  
690 695 700

Asp Cys Trp Glu Pro Val Gln Glu  
705 710

<210> 11

<211> 1830



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 11

|                                                                    |      |
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| gtgtttcgtc gagatgcaca caagagtgag gttgctcatc ggtttaaaga tttgggagaa  | 120  |
| gaaaatttca aagccttggt gttgattgcc tttgctcagt atcttcagca gtgtccattt  | 180  |
| gaagatcatg taaaattagt gaatgaagta actgaatttg caaaaacatg tgttgctgat  | 240  |
| gagtcagctg aaaatttgtga caaatcactt catacccttt ttggagacaa attatgcaca | 300  |
| gttgcaactc ttcgtgaaac ctatggtgaa atggctgact gctgtgcaaa acaagaacct  | 360  |
| gagagaaatg aatgcttctt gcaacacaaa gatgacaacc caaacctccc ccgattgggtg | 420  |
| agaccagagg ttgatgtgat gtgactgct tttcatgaca atgaagagac atttttgaaa   | 480  |
| aaatacttat atgaaattgc cagaagacat cttactttt atgccccgga actccttttc   | 540  |
| tttgctaaaa ggtataaagc tgcttttaca gaatgttgcc aagctgctga taaagctgcc  | 600  |
| tgccgtgtgc caaagctcga tgaacttcgg gatgaaggga aggcttcgtc tgccaaacag  | 660  |
| agactcaagt gtgccagtct ccaaaaattt ggagaaagag ctttcaaagc atgggcagta  | 720  |
| gctcgctga gccagagatt tcccaaagct gagtttgag aagtttccaa gttagtga      | 780  |
| gatcttacca aagtccacac ggaatgctgc catggagatc tgcttgaatg tgctgatgac  | 840  |
| agggcggacc ttgccaaagta tatctgtgaa aatcaagatt cgatctccag taaactgaag | 900  |
| gaatgctgtg aaaaacctct gttggaaaaa tcccactgca ttgccgaagt ggaaaatgat  | 960  |
| gagatgcctg ctgacttgcc ttcattagct gctgattttg ttgaaagtaa ggatgtttgc  | 1020 |
| aaaaactatg ctgaggcaaa ggatgtcttc ctgggcatgt ttttgatga atatgcaaga   | 1080 |
| aggcatcctg attactctgt cgtgctgctg ctgagacttg ccaagacata tgaaaccact  | 1140 |
| ctagagaagt gctgtgccgc tgcagatcct catgaatgct atgccaaaagt gttcgatgaa | 1200 |
| tttaaacctc ttgtggaaga gcctcagaat ttaatcaaac aaaatttgtga gctttttgag | 1260 |
| cagcttgag agtacaaatt ccagaatgcg ctattagttc gttacaccaa gaaagtaccc   | 1320 |
| caagtgtcaa ctccaactct tgtagaggtc tcaagaaacc taggaaaagt gggcagcaaa  | 1380 |
| tgttgtaaac atcctgaagc aaaaagaatg ccctgtgcag aagactatct atccgtgggtc | 1440 |
| ctgaaccagt tatgtgtgtt gcatgagaaa acgccagtaa gtgacagagt caccaaagtc  | 1500 |
| tgacagaaat ccttggtgaa caggcgacca tgcttttcag ctctggaagt cgatgaaaca  | 1560 |
| tacgttccca aagagtttaa tgctgaaaca ttcaccttcc atgcagatat atgcacactt  | 1620 |
| tctgagaagg agagacaaat caagaaacaa actgcacttg ttgagcttgt gaaacacaag  | 1680 |

ZYU.0603.ST25.txt

cccaaggcaa caaaagagca actgaaagct gttatggatg atttcgcagc tttttagag 1740  
aagtgtgca aggctgacga taaggagacc tgctttgccg aggagggtaa aaaacttggt 1800  
gctgcaagtc aagctgcctt aggcttataa 1830

<210> 12

<211> 609

<212> PRT

<213> Homo sapiens

<400> 12

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala  
1 5 10 15

Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala  
20 25 30

His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu  
35 40 45

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val  
50 55 60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp  
65 70 75 80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp  
85 90 95

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala  
100 105 110

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln  
115 120 125

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val  
130 135 140

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys  
145 150 155 160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro  
165 170 175

ZYU.0603.ST25.txt

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys  
180 185 190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu  
195 200 205

Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys  
210 215 220

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val  
225 230 235 240

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser  
245 250 255

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly  
260 265 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile  
275 280 285

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu  
290 295 300

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp  
305 310 315 320

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser  
325 330 335

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly  
340 345 350

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val  
355 360 365

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys  
370 375 380

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu  
385 390 395 400

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys  
405 410 415

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu  
420 425 430

ZYU.0603.ST25.txt

Val Arg Tyr Thr Lys Lys Val Pro Glu Val Ser Thr Pro Thr Leu Val  
435 440 445

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His  
450 455 460

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val  
465 470 475 480

Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg  
485 490 495

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe  
500 505 510

Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala  
515 520 525

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu  
530 535 540

Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys  
545 550 555 560

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala  
565 570 575

Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe  
580 585 590

Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly  
595 600 605

Leu

<210> 13

<211> 600

<212> DNA

<213> Homo sapiens

<400> 13

atgaactgtg tttgccgcct ggtcctgggc gtgctgagcc tgtggccaga tacagctgtc

60

## ZYU.0603.ST25.txt

gcccctgggc caccacctgg cccccctcga gtttccccag accctcgggc cgagctggac 120  
 agcaccgtgc tcctgacctg ctctctcctg gcggacacgc ggcagctggc tgcacagctg 180  
 agggacaaat tcccagctga cggggaccac aacctggatt ccctgcccac cctggccatg 240  
 agtgcggggg cactgggagc tctacagctc ccaggtgtgc tgacaaggct gcgagcggac 300  
 ctactgtcct acctgcggca cgtgcagtgg ctgcgccggg caggtggctc ttccctgaag 360  
 accctggagc ccgagctggg caccctgcag gcccgactgg accggctgct gcgccggctg 420  
 cagctcctga tgtccgcct ggccctgccc cagccacccc cggaccgcgc ggcgccccgc 480  
 ctggcgcccc cctcctcagc ctgggggggc atcagggccg cccacgccat cctggggggg 540  
 ctgcacctga cacttgactg ggccgtgagg ggactgctgc tgctgaagac tcggctgtga 600

&lt;210&gt; 14

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

Met Asn Cys Val Cys Arg Leu Val Leu Val Val Leu Ser Leu Trp Pro  
 1 5 10 15  
 Asp Thr Ala Val Ala Pro Gly Pro Pro Pro Gly Pro Pro Arg Val Ser  
 20 25 30  
 Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr Arg Ser  
 35 40 45  
 Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe  
 50 55 60  
 Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu Ala Met  
 65 70 75 80  
 Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu Thr Arg  
 85 90 95  
 Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp Leu Arg  
 100 105 110  
 Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr  
 115 120 125

ZYU.0603.ST25.txt

Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu Leu Met  
130 135 140

Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala Pro Pro  
145 150 155 160

Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala His Ala  
165 170 175

Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg Gly Leu  
180 185 190

Leu Leu Leu Lys Thr Arg Leu  
195

<210> 15  
<211> 582  
<212> DNA  
<213> Homo sapiens

<400> 15  
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ctgggcctcc cagtcctggg cgccccacca cgctcatct gtgacagccg agtcctggag 120  
aggtacctct tggaggccaa ggaggccgag aatatcacga cgggctgtgc tgaacactgc 180  
agcttgaatg agaatatcac tgtcccagac accaaagtta atttctatgc ctggaagagg 240  
atggagggtcg ggcagcaggc cgtagaagtc tggcagggcc tggccctgct gtcggaagct 300  
gtcctgcggg gccaggccct gttggtcaac tcttcccagc cgtgggagcc cctgcagctg 360  
catgtggata aagccgtcag tggccttcgc agcctcacca ctctgcttcg ggctctgcga 420  
gcccagaagg aagccatctc ccctccagat gcggcctcag ctgctccact ccgaacaatc 480  
actgctgaca ctttccgcaa actcttccga gtctactcca atttcctccg gggaaagctg 540  
aagctgtaca caggggaggc ctgcaggaca ggggacagat ga 582

<210> 16  
<211> 193  
<212> PRT  
<213> Homo sapiens

<400> 16

ZYU.0603.ST25.txt

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu  
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu  
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu  
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu  
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg  
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu  
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser  
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly  
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu  
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile  
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu  
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp  
180 185 190

Arg

<210> 17

<211> 630

<212> DNA

<213> Homo sapiens

ZYU.0603.ST25.txt

<400> 17  
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 ctgtggcaca gtgcaactctg gacagtgcag gaagccaccc ccctgggccc tgccagctcc 120  
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 gcagcgctcc aggagaagct gtgtgccacc tacaagctgt gccaccccga ggagctggtg 240  
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 ctgcagctgg caggctgctt gagccaactc catagcggcc ttttcctcta ccaggggctc 360  
 ctgcaggccc tggaagggat ctcccccgag ttgggtccca ccttggaacac actgcagctg 420  
 gacgtcgccg actttgccac caccatctgg cagcagatgg aagaactggg aatggcccct 480  
 gccctgcagc ccaccagggt tgccatgccg gccttcgcct ctgctttcca gcgccgggca 540  
 ggaggggtcc tagttgcctc ccatctgcag agcttcctgg aggtgtcgta ccgcgttcta 600  
 cgccaccttg cccagccctg agccgaattc 630

<210> 18

<211> 204

<212> PRT

<213> Homo sapiens

<400> 18

Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln  
 1 5 10 15  
 Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro  
 20 25 30  
 Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu  
 35 40 45  
 Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys  
 50 55 60  
 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu  
 65 70 75 80  
 Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser  
 85 90 95  
 Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu  
 100 105 110



ZYU.0603.ST25.txt

Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu  
115 120 125

Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala  
130 135 140

Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu  
145 150 155 160

Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg  
165 170 175

Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu  
180 185 190

Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
195 200

<210> 19

<211> 448

<212> DNA

<213> Homo sapiens

<400> 19  
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cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccgg 120  
cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcac 180  
tcagaaatgt ttgacctcca ggagccgacc tgcctacaga cccgcctgga gctgtacaag 240  
cagggcctgc ggggcagcct caccaagctc aagggcccct tgaccatgat ggccagccac 300  
tacaagcagc actgccctcc aaccccggaa acttctctgtg caaccagat tatcaccttt 360  
gaaagtttca aagagaacct gaaggacttt ctgcttgtca tcccctttga ctgctggggag 420  
ccagtccagg agtgagaccg gccagatg 448

<210> 20

<211> 144

<212> PRT

<213> Homo sapiens

&lt;400&gt; 20

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile  
 1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His  
 20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp  
 35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe  
 50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys  
 65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met  
 85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser  
 100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys  
 115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu  
 130 135 140

&lt;210&gt; 21

&lt;211&gt; 459

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

|                                                                   |     |
|-------------------------------------------------------------------|-----|
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| cccatgaccc agacaacgtc cttgaagaca agctgggtta actgctctaa catgatcgat | 120 |
| gaaattataa cacacttaaa gcagccacct ttgcctttgc tggacttcaa caacctcaat | 180 |
| ggggaagacc aagacattct gatggaaaat aaccttcgaa ggccaaacct ggaggcattc | 240 |
| aacagggctg tcaagagttt acagaacgca tcagcaattg agagcattct taaaaatctc | 300 |
| ctgccatgtc tgcccctggc cacggccgca cccacgcgac atccaatcca tatcaaggac | 360 |
| ggtgactgga atgaattccg gaggaaactg acgttctatc tgaaaaccct tgagaatgcg | 420 |

caggctcaac agacgacttt gagcctcgcg atcttttag

459

&lt;210&gt; 22

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 22

Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu Leu Val Arg Pro  
 1 5 10 15

Gly Leu Gln Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp  
 20 25 30

Val Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln  
 35 40 45

Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln  
 50 55 60

Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe  
 65 70 75 80

Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile  
 85 90 95

Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr  
 100 105 110

Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg  
 115 120 125

Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln  
 130 135 140

Thr Thr Leu Ser Leu Ala Ile Phe  
 145 150

&lt;210&gt; 23

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Cloning primer

<400> 23

gaattcatga agtgggtaac ctttatttcc

30

<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 24

gaattcttat aagcctaagg cagcttgact tgc

33

<210> 25

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 25

catatgaact gtgtttgccg cctggtcc

28

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 26

gatatgtatg acacatttaa ttccc

25

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 27

ggatccatgg ggggtgcacga atgtcc

26

<210> 28

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 28

gaattctcat ctgtcccctg tcctgc

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<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 29

ggatccatgg ctggacctgc cacc

25

<210> 30

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 30

gaattctcag ggctgggcaa ggtggc

26

<210> 31

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Cloning primer

<400> 31

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28

<210> 32

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Cloning primer

<400> 32

gaattctcac tcctggactg gctcc

25

<210> 33

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Cloning primer

<400> 33

ctgccttagg cttacctggg ccaccacctg gcc

33

<210> 34

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 34

tgctcactca cagccgagtc ttcagcagc

29

<210> 35

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 35

ctgccttagg cttaatctgt gacagccgag tcc

33

<210> 36

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 36

cactcgagtc atctgtcccc tgcctgc

28

<210> 37

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 37

ctgccttagg cttaccccc ctgggccctg ccagc

35

<210> 38

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 38

ctcgagtcag ggctgggcaa ggtgg

25

<210> 39

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 39

actccttagg cttagcacc gcccgctcgc ccagc

35

<210> 40

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 40

ctcgagtcac tcctggactg gctcc

25



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